

#5

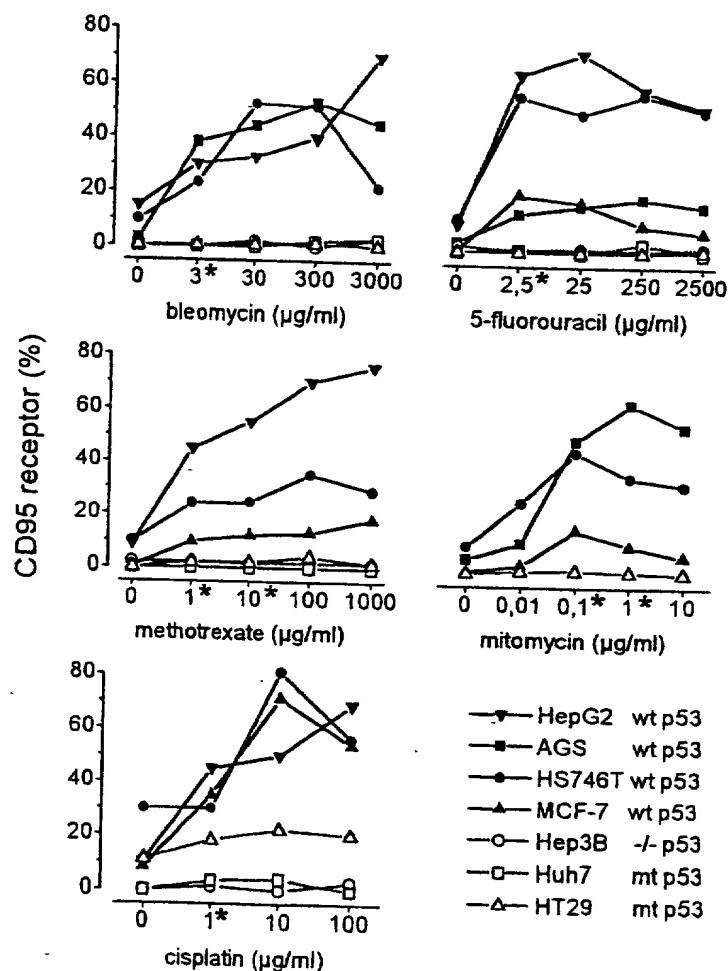


Fig. 1

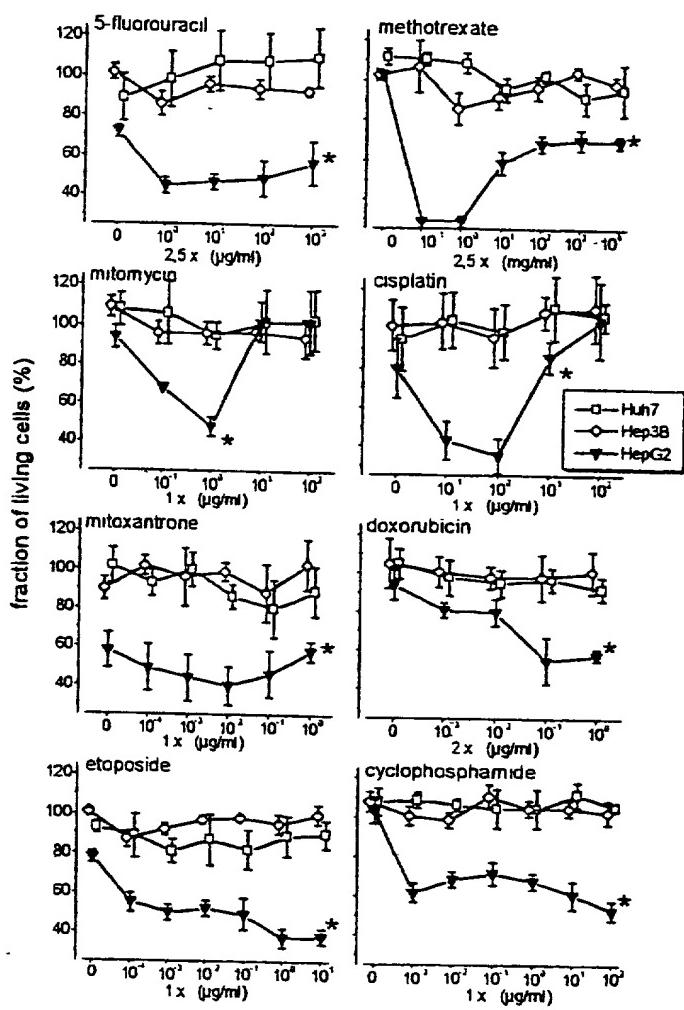


Fig. 2

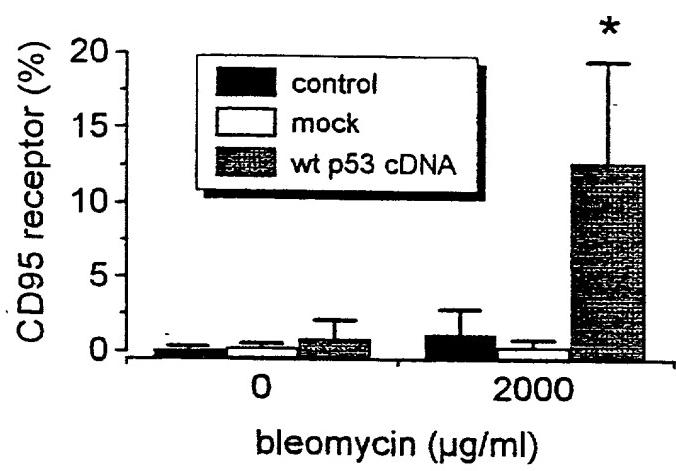


Fig. 3

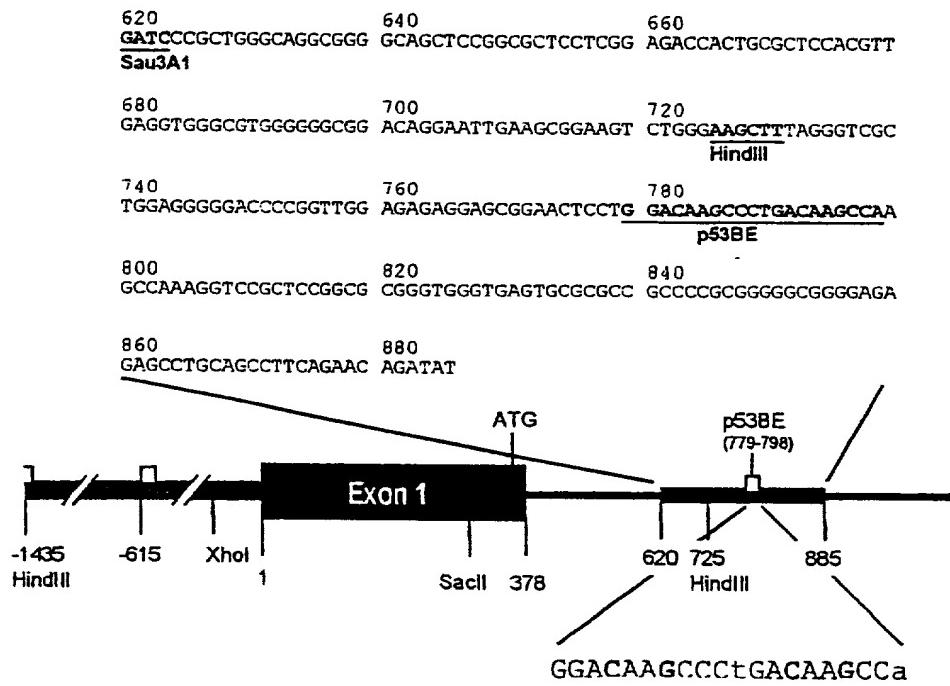


Fig. 4

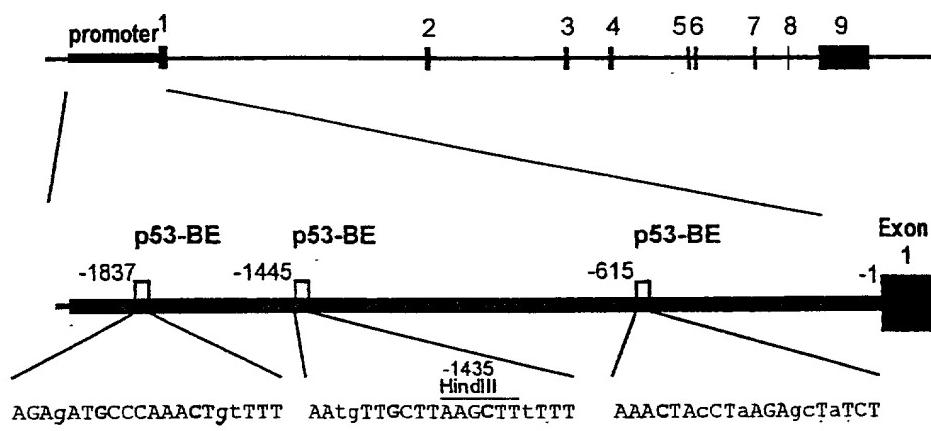


Fig. 5

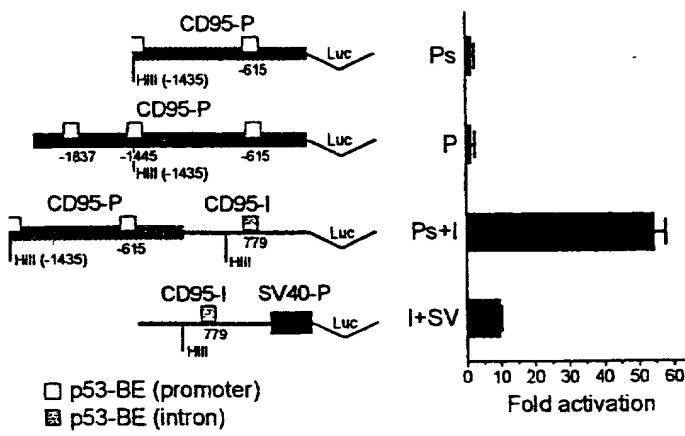


Fig. 6

GATCCCCTGGCAGGCAGGGCAGCTCCGGCGCTCCTCGGAGACCACTGCGCTCCACGTT 60
 1 -----+-----+-----+-----+-----+-----+
 CTAGGGCGACCCGTCCGCCCGTCGAGGCCGAGGAGCCTCTGGTACGCCAGGGTGC

 GAGGTGGCGTGGGGGGCGGACAGGAATTGAAGCGGAAGTCCTGGAAAGCTTAGGGTGC 120
 61 -----+-----+-----+-----+-----+-----+
 CTCCACCCGACCCCCCGCTGCTTAACCTGCCCTCAAGACCCCTCGAAATCCCACG

 <---- 4. P53-BE ---->
 (intron)
 TGGAGGGGGACCCCGTTGGAGAGAGGGAGCGGAACCTCCTGGACAAGCCCTGACAAGCCAA 180
 121 -----+-----+-----+-----+-----+-----+
 ACCTCCCCCTGGGCCAACCTCTCTCGCCTTGAGGACCTGTTGGACTGTTGGTT

 GCCAAAGGTCCGCTCCGGCGCGGGTGGGTGAGTCGCGGCCCGCGGGGGGGAGA 240
 181 -----+-----+-----+-----+-----+-----+
 CGGTTTCCAGCGAGGCCGCCACCCACTCACGCCGCCGGCGCCCCGCCCTCT

 GAGCCTACAGCCTTCAGAACACATATTGCTCATTCTGGAGTTCTCAGACGTAGGAAA 300
 241 -----+-----+-----+-----+-----+-----+
 CTCGGATGTCGGAAGTCTGTGTATAACGAGTAAAGACCGTCAAGAGTCTGCATCCTT

 TAAGTCAGCACCGAACGAGTGGTTAACCGGAGGGCTCGGAAGAACGGCACCTTTCTT 360
 301 -----+-----+-----+-----+-----+-----+
 ATTCACTCGTGGCTTCGTACCCAATTGGCCCTCCGAGCCTTCTTGCCGTGGAAAAGAAA

 CTCGAAAAAGTTATGGGGCTGAATGAGCTTCTGGAGGCTTCTTACGTTTTTATT 420
 361 -----+-----+-----+-----+-----+-----+
 GAGCTTTCAATATAACCCCGACTTACTCGAACGACCTCCGAACAAATGGCAAAAATAA

 GTCACACAGAAAAGGAAACTGCCTTGTCTCCCTTCCGGAAATTCTCTTTAAGACTGTA 480
 421 -----+-----+-----+-----+-----+-----+
 CAGTGTGCTTTCTTGACGGAACAGAGGGAGGCCCTTAAGAGAGAAATTCTGACAT

 AGTCGCTGCCGTGAGTGGTTCTTGTGTTCTGCCCTCTCTTCTTCTTCTTCTTCTT 540
 481 -----+-----+-----+-----+-----+-----+
 TCAGCGACGGACTACCAAAGTAAACAAAACAAAAGACGGGAAGAGAAAGAAGAAAAC

 CCCTTCTTAGCTTGCACCTCCCATGGTATTCTGCTGGCTCCTGCTGGGGTTGGTGG 600
 541 -----+-----+-----+-----+-----+-----+
 GGGAAAGAATCGAACGTGAGGGTACCACTAACAGACGAACCAAGAGGACGCCAACACC

 TACTCGTCCCACCGCACAGAACCCGGCGCTTATTATGGCAAGAAACTTGAGCAGCCT 660
 601 -----+-----+-----+-----+-----+-----+
 ATGAGCAAGGGTGGCGTCTGGCCCGGATAATAACGGTTCTTGAAACTCGTCGGA

 GTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTGCAAGATGGCTAATCAAAGAGACGTG 720
 661 -----+-----+-----+-----+-----+-----+
 CAAAACTTTCAGGGAGCGAGTCTTACGGTCAACGTACCGATTAGTTCTCTGCAC

Fig. 7

2nd half of the
2.p53-BE
(promoter)

AGCTTTTGGCTACATTTTATTGTAAAG
 448 +-----+-----+-----+-----+ 480
 TCGAAAAAACGATGAAAAAATAAACATTTC

 TAAGTTAATAACTCATCTCACTGGGCTATAATGATAAGTATTAAAGTAAGGAAGATC
 481 -----+-----+-----+-----+-----+-----+-----+-----+ 540
 ATTCAAATTATTAGTAGAGTGACCCGATATTACTATTCTATAATTCTATTCTCTAG

 CACATATGTGAGTTGGCTTATAATTCAACACTCAAGAGATACTGATTTGTCAATTGT
 541 -----+-----+-----+-----+-----+-----+-----+-----+ 600
 GTGTATACTCAACGACCGAATTAAGTGTGAGTTCTATGACTAAAACAGTTAACAA

 CCTTCCCCCTTTCTCTCCCTCCATTCTCTCCCTACCTCTCCCTTC
 601 -----+-----+-----+-----+-----+-----+-----+-----+ 660
 GGAAAGGGGAAAAAAAGAGAGAAGGGAGGAAGGTAAGGAAGAAGGGAAATGGAGAGGAAG

 CTTCCCTCACACCCCTTTCTCTCTTTACATTTTTATTTAAATGAACCTTC
 661 -----+-----+-----+-----+-----+-----+-----+-----+ 720
 GAAGGGAGTGTGGGAAAGGAAGGAAGAAAATGTAAAAAAATAAATTACTGAAAAG

 ATTGGAATAGTTTAGGATTCAAAATTTGAGATAATACAGAGAATGCCATA
 721 -----+-----+-----+-----+-----+-----+-----+-----+ 780
 TAAACCTTATCAAATCTAAAGTTTAAACGTCTCTATTATGTCCTACGGGTAT

 TACCATCCTCCTTATCCCCTCTTTGTGTCTATTAGATGCTCAGAGTGTGCACAA
 781 -----+-----+-----+-----+-----+-----+-----+-----+ 840
 ATGGTAGGAGGATAGGTGAAGAAAACAGATAATCACGAGTCTCACACACGTGTT

 GGCTGGCACGCCAGGGTCTTCTCATGGCACTAACAGTCACTGAAAGGTGGAACAGAG
 841 -----+-----+-----+-----+-----+-----+-----+-----+ 900
 CCGACCGTGCAGGTCCCAGAAGGAGTACCGTGTGACAGTGAACCTTCCACCTGTCTC

 ACAAGCCTATCAACACCTACAGACTGGTGTAAAGTGCAGTGCACAGATGCAAAACACAGG
 901 -----+-----+-----+-----+-----+-----+-----+-----+ 960
 TGTTCGGATAGTTGTGGATGTCTGACCACCATTCACGTCACTGTCAGTTGTGTC

 GTGATGGAAAGCCCTCAGGGTAACCTAACCTAGATTGAGGGCCAAACAGGCTCCA
 991 -----+-----+-----+-----+-----+-----+-----+-----+ 1020
 CACTACCTTCGGGAGTCTCCATTGGATTGGATCTAACACTCCGGTTGTCCGAGGT

 GAAGAAAATGTCAACTGAGAGGAAGCCTGAAGGATGAACTGGCTAAGCAAAGGGTTA
 1021 -----+-----+-----+-----+-----+-----+-----+-----+ 1080
 CTCTTACAGTTGACTCTCTCGGACTCTACTTGTCAACCGATTGCGTTCCCAAT

Fig. 8A

TTAATGGTTATTAAATGGGTTGAATCTAATTGGGAAGGGAGAGAGGGTTGCAGAGTGAGGT
 1081 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1140
 AATTACACAATAATTACCAACTTAGATTAACCCCTCCCTCTCCAACGTCTCACTCCA

 GCAGAGCTTGGTGGACATGCCAAGGAATACTGAAACCTTATGTTGTCAGTCTGGAA
 1141 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1200
 CGTCTCGAACACCCTGCTACGGTTCCCTATGACTTTGGAAATCACACAGGTCAGACCTT

 CTGCATCCAAATTCAAGGTTCACTGATGTCATTATCCAAACATACCTCTGTAAAATT
 1201 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1260
 GACGTAGGTTAAGTCCAAGTCATTACTACAGTAATAGGTTGTATGGAAGACATTTAA

←--- 3.p53-B2 ---→
 (promoter)

CATGCTAAACTACCTAAGAGCTATCTACCGTTCCAAGCAATAGTGACTTTGAACAGTGT
 1261 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1320
 GTACGATTTGATGGATTCTCGATAGATGGCAAGGTTCTGTATCACTGAAACTTGTCA

 TCACCAAGCAGCAAAGAATTACAAGATTTTTAAAGAAAATTGCCAGGAAATAAT
 1321 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1380
 AGTGGTCTCGTCTTCTTAATGTTCTAAAAAAAATTCTTTAACCGGTCTTATTA

 GAGTAACGAAGGACAGGAAGTAATTGTGAATGTTAATATAGCTGGGCTATGCGATTG
 1381 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1440
 CTCATTGCTTCCGTCTTCATTAACACTACAAATTATATCGACCCGATACGCTAAC

 GCCTTAAGTTGTTAGCTTGTCTTGAGAAAATAAAACTTAAGGGGCCCTCCCTTT
 1441 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1500
 CGAATTCAACAATCGAAACAAAAGGAGAACTCTTATTTGATTCCCCGGGAGGGAAA

 CAGAGCCCTATGGCGAACATCTGTACTTTCATATGGTTAATGTCCATTCCAGGAAC
 1501 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1560
 GTCTCGGGATACCGCGTTGTAGACATGAAAAGTATACCAATTGACAGGTAAAGGTCTTG

 GTCTGTGAGCCTCTCATGTTGAGCCACAAACATGGACAGCCAGTCAAATGCCCGCAAG
 1561 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1620
 CAGACACTCGGAGAGTACAACGTCGGTGTACCTGTGGGTCAAGTTACGGGGCGTC

 TCTTCTCTGAGTGACTCCAGCAATTAGCCAAGGCTCTGTACCCAGGCAGGACCTCTGC
 1621 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1680
 AGAAAGAGACTCACTGAGGTGTTAATCGGTTCCGAGGAATGGTCCGTCTGGAGACG

 GCTCTGAGCTCCATTCTCTCAAGACCTCCCCACTTCCCAGGTTGAACTACAGCAGAA
 1681 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1740
 CGAGACTCGAGGTAAAGGAGTTCTGGAGGGGTGAAGGGTCAACTTGTGTCGTCTT

 GCCTTAGAAAGGGCAGGAGGCCGCTCTGAGGTCTCACCTGAAGTGAGCATGCCAGC
 1741 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1800
 CGGAAATCTTCCCGTCTCCGGCCGAGAGCTCCAGGAGTGGACTTCACTCGTACGGTC

 CACTGCAGGAACGCCCGGGACAGGAATGCCATTGTGCAAGCAACCTGACTCCTCC
 1801 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1860
 GTGACGTCTTGCAGGGCCCTGTCTTACGGTAAACACGTTGCTGGACTGAGGAAGG

 TCACCCCTGACTTCTCCCCCTCCCTACCCGCGCAGGCCAAGTTGCTGAATCAATGGAGC
 1861 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1920
 AGTGGGACTGAAAGGGGGAGGGATGGCGCGTCCGGTTCAACGACTTAGTTACCTCG

Fig. 8B

CCTCCCCAACCGGGGTTCCCAAGCGAGGCTTCCATCCTCCGACCACCGGGC
 1921 -----+-----+-----+-----+-----+-----+ 1980
 GGAGGGGTTGGGCCCGAAGGGTCGCTCCGAAGGAAGGTAGGAGGACTGGTGGCCCCG

 TTTTCGTGAGCTCGTCTGATCTCGCGAAGAGTGACACACAGGTGTTAAAGACGCTT
 1981 -----+-----+-----+-----+-----+-----+ 2040
 AAAAGCACTCGAGCAGAGACTAGAGCGCGTCTCACTGTGTCCACAAGTTCTGCAGA

 CTGGGGAGTGGGAAGCGGTTACGAGTGACTTGGCTGGACGCTCAGGGCGGGACTG
 2041 -----+-----+-----+-----+-----+-----+ 2100
 GACCCCTCACTCCCTCGCAAATGCTCACTGAACCGACCTCGGAGTCCCCTGGACTG

 GCACGGAACACACCCCTGAGGCCAGCCCTGGCTGCCAGCGGAGCTGCCTCTCCGC
 2101 -----+-----+-----+-----+-----+-----+ 2160
 CGTGCCTTGTGTGGACTCCGGTCGGGACCGACGGTCCGCTCGACGGAGAAGAGGGCG

 GGACATGTACAGAGCTCGAGAAGTACTAGTGGCACGTGGCCGTGCACCTTAAGCTTA
 2161 -----+-----+-----+-----+-----+-----+ 2220
 CCTGTACATGTCTCGAGCTTCATGATCACCGTGCACCCGGCACGTGGAATTGAAAT

←---4.p53-BE---
(intron)

GGGTCGCTGGAGGGGGACCCCGGTGGAGAGAGGGAGCGGAACCTCTGGACACCCCTGAC
 2221 -----+-----+-----+-----+-----+-----+ 2280
 CCCAGCGACCTCCCCCTGGGCCAACCTCTCGCCTTGAGGACCTGTCGGGACTG

 →

 AAGCCAAGCAAAGGTCCGCTCCGGCGCGGGTGGGTGAGTGGCGGCCGCCGGGGGC
 2281 -----+-----+-----+-----+-----+-----+ 2340
 TTCCGGTTCGGTTCCAGCGAGGCGCGCCACCCACTCACCGCGGCCGGCGCCCCCG

 GGGGAGAGAGCCTGCAGCCTTCAGAACAGATATTGCTCATTTCTGGCAGTTCTCAGACG
 2341 -----+-----+-----+-----+-----+-----+ 2400
 CCCCTCTCGGACGTCGGAAGTCTTGTCTATAACGAGTAAAAGACCGTCAAGAGTC

 TAGGAAATAAGTCAGCACCGAAGCAGTGGTTAAGCCGGAGGGCTCGGAAGAACGGCACCT
 2401 -----+-----+-----+-----+-----+-----+ 2460
 ATCCCTTATTCACTGGCTTCCACCAATTGGCCTCCGAGCCTTGTGCCGTGGA

 TTTCTTCTCGAAAAGTTATATGGGGCTGAATGAGCTCTGGAGGCTGTTACCGTT
 2461 -----+-----+-----+-----+-----+-----+ 2520
 AAAGAAAGAGCTTTCAATATACCCCGACTTACTCGAACGACCTCCGAAACAATGCCA

 TTTTATTGTACACAGAAAAGGAAACTGCCTTGTCTCCCTCCGGAAATTCTCTTTAA
 2521 -----+-----+-----+-----+-----+-----+ 2580
 AAAATAACAGTGTGCTTTCTTGACGGAACAGAGGGAGGCCCTAACGAGAGAAATT

 GACTGTAAGTCGCTGCCTGAGTGGTTTCAATTGTTGTTCTGCCCTCTCTTCT
 2581 -----+-----+-----+-----+-----+-----+ 2640
 CTGACATTCAAGCGACGGACTCACCAAGTAAAACAAAAGACGGGAAGAGAAAGA

 TCTTTGCCCTTCTTASCTTGCACTCCCATGGTGTGATTCTGCTTGGCTCTGCTGGGG
 2641 -----+-----+-----+-----+-----+-----+ 2700
 AGAAAACGGGAAAGAACGTGAGGGTACCAACTAAAGACGAACCGAGGGACGACCCC

Fig. 8C

2701 TTGGTGGTACTCGTCCCCACCGCACAGAACCCGGCGCTATTATTGGCCAAGAAACTTGA 2760
AACCACCATGAGCAAGGGTGGCGTGTCTGGGCCGCGATAATAACCGGTTCTTGAACT

2761 GCAGCCTGTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTTCAGATGGCTAATCAAAG 2820
CGTCGGACAAAACTTTCAGGGAGCGAGTCTTACGGTCGAACGTCTACCGATTAGTTTC

2821 AGACGTG 2827
TCTGCAC

Fig. 8D

<---- 1.p53-BE --

1 TGAGGACTCTCAGGAATATGCTGGTAAAATAAAAAACCTTAGAGATGCCAACTGT
1 ACTCCTGAGAGTCCTTATACGACCATTATTTATTGGAAATCTCTACGGGTTGACA 60

-->

61 TTTCCCCAGAACACCAGCATTCAATTAGGTGTTCAATAGATTCTCAAAGGATTCCA
61 AAAGGGGCTTGTGGTCGTAAGTAATCCACAAGTAAGTTATCTAAGAAGTTCTAAGGT 120

121 AAGGCAAAGAAGTTGGGAACAGTATATATAATTACCAACCCTTGACATTAGCATAC
121 TTCCGTTCTCAAACCCCTGTCAATATATAATTGGTTGGAACTGTAATCGTATG 180

181 TAAGGGCCCTGAGAAGTTGGATTAAGAAAGTTCAAATAAAGTAACCCAGAATTTC
181 ATTCCCGGGACTCTCAAAACCTAATTCTTCAAAGTTAATTCAATTGGGTCTTAAAA 240

241 CTAAGATTATTTGACCATGAAACATATGTCCTCCCACAAAGCACATATTCTATCTCCTT
241 GATTCTAATAAACTGGTACTTTGTATACAGAGGGGTGTTCTGTATAAGGATAGAGGA 300

301 GAACTTGAGGATAATTAGACGTACGTGGTAGAGGGTAGGGGAAGGGGTATGGCATAGA
301 CTTGAECTCCTATTAAATCTGCATGCACCCATCTCCATCCCCCTCCCCATACCGTATCT 360

361 AAGAGCAGGACCTGGGAGCAAGAATATCTAAGTTAATTCTGACTCTGCTATTATTA
361 TTCTCGTCTGGAACCCCTCGTTATAGCTAAAGGACTGAGACGATAATAAT 420

<---- 2.p53-BE ---->

421 ACTAACCATCTTGCCTAAGCTTTGGCTACATTTTTATTGTAAAG
421 TGATTGGTAGAACGGTTACAACGAATTGAAAAACCGATGTAAAAATAAACATTTC 480

481 TAAGTTAATAATCACTCATCTACTGGCTATAATGATAAGTTAAAGTAAGGAAGATC
481 ATTCAAATTATTAGTGAGTAGAGTGACCCGATATTACTATAATTCTCTCTAG 540

541 CACATATGTGAGTTGCTGGCTATAATTCAACACTCAAGAGATACTGATTGTCAATTGT
541 GTGTATACACTCAACGACCGAATTAAGTGTGAGTTCTATGACTAAACAGTTAAC 600

601 CCTTTCCCTTTTCTCTTCCCTCCATTCTTCCATTCTACCTCTCCTTC
601 GGAAAGGGAAAAAAAGAGAGAAGGGAGGAAGGTAAAGGAAGAAGGGATGGAGAGGAAG 660

Fig. 9A

09834697 09834698

CTTCCCTCACACCCCTTCCCTCTTTACATTTTATTAAATGAACTTTC
 661 -----+-----+-----+-----+-----+-----+-----+-----+ 720
 GAAGGGAGTGTGGGAAAAGGAAGGAAGAAAAATGTAAAAAATAATTACTTGAAAAG

 ATTTGGAATAGTTAGGATTCAAAAATTGCAGAGATAATACAGAGAATGCCATA
 721 -----+-----+-----+-----+-----+-----+-----+-----+ 780
 TAAAACCTTATCAAATCTAAAGTTTAAACGTCTATTATGCTCTACGGGTAT

 TACCATCCTCCTTATCCCACCTCTTTGTCTATTAGATGCTCAGAGTGTGACAA
 781 -----+-----+-----+-----+-----+-----+-----+-----+ 840
 ATGGTAGGAGGAATAGGGTGAGAAAAACACAGATAATCTACGAGTCTCACACACGTGTT

 GGCTGGCACGCCAGGGCTCCTCATGGCACTAACAGTCTACTGAAAGGTGGAACAGAG
 841 -----+-----+-----+-----+-----+-----+-----+-----+ 900
 CGCACCGTGGGGTCCCAGAAGGAGTACCGTATTGTCAGATGACTTTCCACCTGTCTC

 ACAAGCCTATCAACACCTACAGACTGGTGGTAAGTGCAGTGACAGATGCAAAACACAGG
 901 -----+-----+-----+-----+-----+-----+-----+-----+ 960
 TGTTCGGATAGTTGTGGATGTTCTGACCACATTACGGTCACTGTCTACGTTGTGTC

 GTGATGGAAAGCCCTCAGGGGGTAACCTAACCTAGATTGAGGGCCAAACAGGCTCCA
 991 -----+-----+-----+-----+-----+-----+-----+-----+ 1020
 CACTACCTTCGGGAGTCCTCCATTGGATTGGATCTAAACTCCGGTTGTCCGAGGT

 GAAGAAAATGTCACGTGAGAGGAAGCCTGAAGGATGAACAGTGGCTAAGCAAAGGGTTA
 1021 -----+-----+-----+-----+-----+-----+-----+-----+ 1080
 CTCTTTTACAGTTGACTCTCCTCGACTCTACTTGTCAACCGATTGTTCCAAAT

 TTAATGTGTTATTAAATGGGTGAATCTAATTGGGAAGGGAGAGGGTTGCAGAGTGGAGGT
 1081 -----+-----+-----+-----+-----+-----+-----+-----+ 1140
 AATTACACAATAATTACCCAACTTAGATTAACCCCTCCCTCTCCAAACGTCTCACTCCA

 GCAGAGCTTGGTGGACGATGCCAAGGAATACTGAAACCTTGTGTCCAGTCTGGAA
 1141 -----+-----+-----+-----+-----+-----+-----+-----+ 1200
 CGTCTGAACCAACCTGCTACGGTTCTTATGACTTGGAAATCACACAGGTGAGACCTT

 CTGCATCCAATTCAAGGTCAGTAATGATGTCATTATCCAAACATACTTCTGTAAAATT
 1201 -----+-----+-----+-----+-----+-----+-----+-----+ 1260
 GACGTAGGTTAAGTCCAAGTCATTACTACAGTAATAGGTTGTATGGAAGACATTAA

 <---- 3.p53-BE ---->

CATGCTAAACTACCTAACAGAGCTATCACCGTCAAAGCAATAGTGACTTGAACAGTGT
 1261 -----+-----+-----+-----+-----+-----+-----+-----+ 1320
 GTACGATTTGATGGATTCTCGATAGATGGCAAGGTTCGTTATCACTGAAACTTGTCA

 TCACCAAGCAGGAAAGAATTACAAGATTTTTAAAGAAAATTGCCAGGAATAAT
 1321 -----+-----+-----+-----+-----+-----+-----+-----+ 1380
 AGTGGTCTCGCTTCTTAAATGTTCTAAACATTATCGACCCGATACGCTAAAC

 GAGTAACGAAGGACAGGAAGTAATTGTAATGTTAATATAGCTGGGCTATGGGATTG
 1381 -----+-----+-----+-----+-----+-----+-----+-----+ 1440
 CTCATTGCTTCTGCTTCAATTAAACATTACAAATTATCGACCCGATACGCTAAAC

 GCCTTAAGTTAGCTTCTTCTTGTGAGAAAATAAAACTAAGGGCCCTCCCTTT
 1441 -----+-----+-----+-----+-----+-----+-----+-----+ 1500
 CGAATTCAACAATCGAAACAAAGGAGAACTCTTATTTGATTCCCCGGGAGGGAAA

 CAGAGCCCTATGGCGAACATCTGACTTTCATATGGTTAATGTCATTCCAGGAAC
 1501 -----+-----+-----+-----+-----+-----+-----+-----+ 1560
 GTCTCGGGATACCGCGTTGAGACATGAAAAGTATACCAATTGACAGGTAAAGTC

Fig. 9B

GTCTGTGAGCCCTCATGTTGCAGGCCAACATGGACAGCCCAGTCAAATGCCCGCAAG
 1561 -----+-----+-----+-----+-----+-----+-----+-----+ 1620
 CAGACACTCGGAGAGTACACGTCGGTGTACCTGTCGGTCAGTTACGGGGCGTTC

 TCTTTCTCTGAGTGACTCCAGCAATTAGCCAAGGGCTCTGTACCCAGGCAGGACCTCTGC
 1621 -----+-----+-----+-----+-----+-----+-----+-----+ 1680
 AGAAGAGAGACTCACTGAGGTGTTAACCGGTTCCGAGGAATGGGTCCTGGAGACG

 GCTCTGAGCTCCATTCTCCTTAAGACCTCCCCAACTTCCAGGTTGAACATACAGCAGAA
 1681 -----+-----+-----+-----+-----+-----+-----+-----+ 1740
 CGGAACTCGAGGTAAGAGGAAGTTCTGGAGGGGTTGAAGGGTCAAACGTGATGTCGTT

 GCCTTAGAAAGGGCAGGAGGCCGCTCGAGGTCTCACCTGAAGTGAGCATGCCAGC
 1741 -----+-----+-----+-----+-----+-----+-----+-----+ 1800
 CGGAAATCTTCCCGTCTCCGGCCGAGAGCTCCAGGAGTGGACTTCACTCGTACGGTCG

 CACTGCAGGAACGCCCCGGGACAGGAATGCCATTGTCGAACGAACCTGACTCCTCC
 1801 -----+-----+-----+-----+-----+-----+-----+-----+ 1860
 GTGACGTCTTGCGGGGCCCTGTCTTACGGTAAACACGTTGCTTGGACTGAGGAAGG

 TCACCCCTGACTCTCCCCCTCCCTACCCGGGGCAGGCCAAGTTGCTGAATCAATGGAGC
 1861 -----+-----+-----+-----+-----+-----+-----+-----+ 1920
 AGTGGGACTGAAGAGGGGGAGGGATGGGCGCGTCCGGTCAACGACTTAGTTACCTCG

 CCTCCCCAACCGGGCGTCTCCAGCGAGGCTCTTCCATCCCTGACCACCGGGC
 1921 -----+-----+-----+-----+-----+-----+-----+-----+ 1980
 GGAGGGGTTGGGCCGCAAGGGTCGCTCCGAAGGAAGGGTAGGAGGACTGGTGGCCCG

 TTTTCGTGAGCTCGTCTCTGATCTCGCGAAGAGTGACACACAGGTGTTCAAAGACGCTT
 1981 -----+-----+-----+-----+-----+-----+-----+-----+ 2040
 AAAAGCACTCGAGCAGAGACTAGAGCGCGTCTCACTGTGTGTCACAAGTTCTGCGAA

 CTGGGGAGTGAGGGAGCGGTTACGAGTGACTTGGCTGGAGCCTCAGGGCGGGCACTG
 2041 -----+-----+-----+-----+-----+-----+-----+-----+ 2100
 GACCCCTCACTCCCTGGCAAATGTCACTGAACCGACCTCGGAGTCCCCCGGTGAC

 GCACGGAACACACCCCTGAGGCCAGCCCTGGCTGCCAGGCCAGCTGCCCTTCTCCGC
 2101 -----+-----+-----+-----+-----+-----+-----+-----+ 2160
 CGTGCCTTGTTGGACTCCGGTCGGACCGACGGTCCGCTGACGGAGAAGAGGGCG

 GGACATGTACAGAGCTCGAGAAGTACTAGTGGCCACGTGGCCGTGACCTTAAGCTTTA
 2161 -----+-----+-----+-----+-----+-----+-----+-----+ 2220
 CCTGTACATGTCTCGAGCTTCAATGATCACCGGTGCACCCGGCACGTGGAATTGAAAT

<---- 4.p53-BE
(intron) ---->

GGGTCGCTGGAGGGGACCCGGTTGGAGAGAGGAGCGGAACCTGGACAAGCCCTGAC
 2221 -----+-----+-----+-----+-----+-----+-----+-----+ 2280
 CCCAGCGACCTCCCCCTGGGCCAACCTCTCTCGCCTTGAGGACCTGTTGGACTG

AAGCCAGCAAAGGTCCCTCCGGCGGGTGGTGAGTGCGCCGCCGCCCCGGGG
 2281 -----+-----+-----+-----+-----+-----+-----+-----+ 2340
 TTGGTTGGTTCCAGGCCAGGCCGCCACCCACTCACGCGCGGGCGCCCCCG

GGGGAGAGAGCCTGCAGCCTCAGAACAGATAATTGCTATTCTGGCAGTTCTCAGACG
 2341 -----+-----+-----+-----+-----+-----+-----+-----+ 2400
 CCCCTCTCGGACGTGCGAACGTTGCTATAACGAGTAAAAGACCGTCAAGAGTCTGC

Fig. 9C

2401 TAGGAAATAAGTCAGCACCGAACGCAGTGGTTAAGCCGGAGGGCTCGGAAGAACGGCACCT + 2460
 ATCCTTATTCAAGTCGTGGCTCGTCACCAATT CGGCCTCCGAGCCTTCTGCCGTGGA

 2461 TTTCTTCTCGAAAAAGTTATATGGGGCTGAATGAGCTTCTGGAGGCTTACCGTT + 2520
 AAAGAAAGAGCTTTCAATATAACCCCCGACTTACTCGAAGACCTCCGAACAATGGCAA

 2521 TTTTATGTCACACAGAAAAGGAAC TGCCCTGCTCCCTCCGGAAATTCTCTCTTAA + 2580
 AAAATAACAGTGTCCTTCCTTGACGGAACAGAGGGAAAGGCCCTTAAGAGAGAAATT

 2581 GACTGTAAGTCGCTGCCTGAGTGGTTCACTTTGTTTCTGCCCTCTCTTCT + 2640
 CTGACATTCAAGCGACGGACTCACCAAGTAAAACAAAACAAAAGACGGGAAGAGAAAGA

 2641 TCTTTGCCCTTCTTAGCTTGCACTCCCATGGTATTCTGCTTGGTCTCCTGCTGGGG + 2700
 AGAAAAACGGGAAAGAATCGAACGTGAGGGTACCACTAAAGACGAACCAGAGGGACGACCCC

 2701 TTGGTGGTACTCGTCCCACCGCACAGAACCCGGCGCTATTGGCCAAGAAACTTGA + 2760
 AACCAACATGAGCAAGGGTGGCGTGTCTGGGCCGCGATAATAACCGTTCTTGAAC

 2761 GCAGCCTGTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTGCAGATGGCTAATCAAAG + 2820
 CGTCGGACAAAACCTTCAAGGGAGCGAGTCTTACGGTCGAACGTCTACCGATTAGTTTC

 2821 AGACGTG + 2827
 TCTGCAC

Fig. 9D

<---- 1. p53-BE ---
(promoter)

TGAGGACTCTCAGGAATATGCTGGTAAAATAAAAATAACCTTAGAGATGCCAAACTGT
 1 -----+-----+-----+-----+-----+-----+-----+ 60
 ACTCCCTGAGAGTCCTTATACGACCATTATTTATTGAAATCTCTACGGGTTGACA

 -->

 TTTCCCCAGAACACCAAGCATTCAATTAGGTGTCATTCAATAGATTCTCAAAGGATTCCA
 61 -----+-----+-----+-----+-----+-----+-----+ 120
 AAAGGGGCTTGTTGGTCGAAGTAATCCACAAGTAAGTTATCTAAGAAGTTCTAAGGT

 AAGGCAAAAGAAGTTGGGAAACAGTATATATAATTACCCAAACCCTTGACATTAGCATAC
 121 -----+-----+-----+-----+-----+-----+-----+ 180
 TTCCGTTCTCAACCCCTTGTCAATATATAATTATGGTTGGGAAACTGTAATCGTATG

 TAAGGGCCCTGAGAAGTTGGATTAAGAAGTTCAAATTAAAGTAACCCAGAATT
 181 -----+-----+-----+-----+-----+-----+-----+ 240
 ATTCCCAGGACTCTCAAAACCTAATTCTCAAAAGTTAATTCAATTGGGTCTTAAAA

 CTAAGATTATTTGACCATGAAACATATGTCCTCCCACAAAGCACATATTCTATCTCCTT
 241 -----+-----+-----+-----+-----+-----+-----+ 300
 GATTCTAATAAACTGGTACTTTGTATAAGAGGGGTGTTCTGTATAAGGATAGAGGAA

 GAACCTTGAGGATAATTAGACGTACGTGGTAGAGGGTAGGGGAAGGGGTATGGCATAGA
 301 -----+-----+-----+-----+-----+-----+-----+ 360
 CTTGAACCTCTTAAATCTGCATGCACCCATCTCCATCCCTCCCATACCGTATCT

 AAGAGCAGGACCTGGGAGCAAGAATATCTAAGTTAATTCTGACTCTGCTATTATA
 361 -----+-----+-----+-----+-----+-----+-----+ 420
 TTCTCGTCCCTGGAACCCCTCGTTCTATAGATTCAAATTAGGACTGAGACGATAAAAT

<---- 2. p53-BE ---->
(promoter)

ACTAACCATTTGCCAATGTTGCTTAAGCTTTGGCTACATTTTTATTGAAAG
 421 -----+-----+-----+-----+-----+-----+-----+ 480
 TGATTGGTAGAACGGTTACACGPAATCGAAAAACCGATGAAAAAAATAACATTC

 TAAGTTAATAATCACTCATCTCACTGGCTATAATGATAAGTATTAAAGTAAGGAAGATC
 481 -----+-----+-----+-----+-----+-----+-----+ 540
 ATTCAAATTATTAGTGAGTAGAGTGACCCGATAATTACTATTCTATAATTCAATTCTCCTCTAG

 CACATATGTGAGTTGGCTTATAATTCAACTCAAGAGATACTGATTTGTCAATTGT
 541 -----+-----+-----+-----+-----+-----+-----+ 600
 GTGTATACACTCAACGACCGAATATTAGTGAGTTCTCTATGACTAAAACAGTTAAC

 CCTTTCCCTTTCTCTCTCCCTCCATTCTCTTCCCTACCTCTCCTTC
 601 -----+-----+-----+-----+-----+-----+-----+ 660
 GGAAAGGGAAAAAGAGAGAAGGGAGGAAGGTAAGGAAGAAGGAATGGAGAGGAAG

 CTTCCCTCACACCCCTTCCCTCTTACATTATTAAATGAACTTTTC
 661 -----+-----+-----+-----+-----+-----+-----+ 720
 GAAGGGAGTGTGGGAAAGAGAAGGAAGAAAATGAAAAAAATAATTACTTGAAAAG

 ATTTTGGAAATAGTTTAGGATTCAAAATTTGCAGAGATAATACAGAGAATGCCATA
 721 -----+-----+-----+-----+-----+-----+-----+ 780
 TAAAACCTTATCAAAATCTAAAGTTAAACGTCTATTATGTCCTACGGGTAT

Fig. 10A

TACCATCCCTTATCCCACCTCTTTGTCATTAGATGCTCAGAGTGTGCAACAA
 781 +-----+-----+-----+-----+-----+-----+-----+-----+ 840
 ATGGTAGGAGGAATGGGTGAAGAAAAACACAGATAATCTACGAGTCTCACACACGTGTT

 GGCTGGCACGCCAGGGCTTCTCATGGCACTAACAGTCTACTGAAAGGTGGAACAGAG
 841 +-----+-----+-----+-----+-----+-----+-----+-----+ 900
 CCCGACCGTGCAGGGTCCCAGAAGGAGTACCGTGATTGTCAGATGACTTCCACCTGTCTC

 ACAAGCCTATCAACACCTACAAGACTGGTGGTAAGTGCAGTGACAGATGCAAAACACAGG
 901 +-----+-----+-----+-----+-----+-----+-----+-----+ 960
 TGTTCGGATAGTGTGGATGTTCTGACCACATTCACTGACTGTCTACGTTGTGTC

 GTGATGAAAGCCCTCAGGAGGGTAACCTAACCTAGATTGAGGGCCAAACAGGCTCCAG
 961 +-----+-----+-----+-----+-----+-----+-----+-----+ 1020
 CACTACCTTTCGGGAGTCTCCCATGGATTGGACTAAACTCCGGGTGTCGAGGTC

 AAGAAAATGTCAACTGAGAGGAAGCCTGAAGGATGAACAGTGGGCTAAGCAAAGGGTTAT
 1021 +-----+-----+-----+-----+-----+-----+-----+-----+ 1080
 TTCTTTTACAGTGAECTCTCCCTCGACTTCTACTTGTCAACCGATTGCTTCCAAATA

 TAATGTGTTATAATGGGTTGAATCTAATTGGGAAGGGAGAGAGGTTGCAGAGTGAGGTG
 1081 +-----+-----+-----+-----+-----+-----+-----+-----+ 1140
 ATTACACAATAATTACCCAACCTAGATTAAACCCCTCCCTCTCCAACGTCCTCACTCCAC

 CAGAGCTTGGTGGACGATGCCAAGGAATACTGAAACCTTTAGTGTGTCAGTCGGAAC
 1141 +-----+-----+-----+-----+-----+-----+-----+-----+ 1200
 GTCTCGAACCCACTGCTACGGTTCTTATGACTTGGAAATCACACAGGTAGACCTTG

 TGCATCCAATTCAAGGTTCACTGATGTCATTATCCAAACATACCTTCTGAAAATTTC
 1201 +-----+-----+-----+-----+-----+-----+-----+-----+ 1260
 ACGTAGGTTAACTCAAGTCATTACTACAGTAATAGGTTGTATGGAAGACATTAAAG

 <---- 3.p53-BE ---->
 (promoter)

 ATGCTAAACTACCTAACGAGCTATCTACCGTTCAAAGCAATAGTGACTTTGAACAGTGTT
 1261 +-----+-----+-----+-----+-----+-----+-----+-----+ 1320
 TACGATTGATGGATTCTCGATAGATGCCAAGGTTCTTATCACTGAAAATTGTCACAA

 CACCAGAGCACGAAAGAATTACAAGATTTTTAAAGAAAATTGCCAGGAAATAATG
 1321 +-----+-----+-----+-----+-----+-----+-----+-----+ 1380
 GTGGTCTCGTCTTCTTAATGTTCTAAACAAAAATTCTTTAACCGGTCTTATTAC

 AGTAACGAAGGACAGGAAGTAATTGTAATGTTAAATATAGCTGGGGCTATGCGATTGG
 1381 +-----+-----+-----+-----+-----+-----+-----+-----+ 1440
 TCATTGCTTCCTGCTTCTCAAAACTACAAATTATATGACCCCCGATCGCTAAACC

 CTTAAGTTGTTAGCTTGTGTTCTCTTGAGAAATAAAAACAAAGGGCCCTCCCTTTTC
 1441 +-----+-----+-----+-----+-----+-----+-----+-----+ 1500
 GAATTCAACAAATCGAAACAAAGGAGAACTCTTATTGTTGATCCCCGGAGGGAAAAG

 AGAGCCTTATGGCGAACATCTGACTTTCTATGGTTACTGTCCTTCAGAAACG
 1501 +-----+-----+-----+-----+-----+-----+-----+-----+ 1560
 TCTCGGAATACCGCGTTGTAGACATGAAAAGTACCAATTGACAGGTAAAGGTTCTTC

 TCTGTGAGGCCCTCATGTTGCAGGCCAACATGGACAGGCCAGTCAGTCAATGCCCGCAAGT
 1561 +-----+-----+-----+-----+-----+-----+-----+-----+ 1620
 AGACACTCGGAGAGTACAACGTCGGTGTGACCTGTCGGGTCACTTACGGGGCGTTCA

 CTTCTCTGAGTGAATCCAGCAATTAGCCAAGGCTCTGTACCCAGGCAGGACCTCTGCG
 1621 +-----+-----+-----+-----+-----+-----+-----+-----+ 1680
 GAAAAGAGACTCACTGAGGTCGTTAATCGTTCCGAGGACATGGGTCGCTGGAGACCC

 CTCTGAGCTCCATTCTCTCAAGACCTCCCCAACCTCCCAGGTTGAACTACAGCAGAAG
 1681 +-----+-----+-----+-----+-----+-----+-----+-----+ 1740
 GAGACTCGAGGTAAGAGGAAGTCTGGAGGGGTTGAAGGGTCAACTTGTGTCGCTTC

Fig. 10B

CTTTAGAAAGGGCAGGAGGCCGCTCGAGGTCTCACCTGAAGTGAGCATGCCAGCC
 1741 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1800
 GGAAATCTTCCCCTCCGGCCAGAGCTCCAGGAGTGGACTTCACTCGTACGGTCGG

 ACTGCAGGAACGCCCCGGGACAGGAATGCCATTGTGCAACGAACCTGACTCCTCCT
 1801 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1860
 TGACGTCTGGGGCCCTGTCTTAACGGTAAACACGTTGTTGGACTGAGGAAGGA

 CACCCCTGACTTCTCCCCCTCCCTACCCGCGCAGGCCAAGTTGCTGAATCAATGGAGCC
 1861 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1920
 GTGGGACTGAAGAGGGGGAGGGATGGCGCGTCCGGTCAACGACTTAGTTACCTCGG

 CTCCCCAACCCGGGCGTTCCCAGCGAGGCTTCCCATCCTCTGACCACCAGGGCT
 1921 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1980
 GAGGGGTTGGGCCGCAAGGGGTCGCTCGAAGGAAGGGTAGGAGGACTGGTGGCCCGA

 TTTCGTGAGCTCGTCTGTATCTCGCCAAGAGTGACACACAGGTGTTCAAAGACGCTTC
 1981 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2040
 AAAGCACTCGAGCAGAGACTAGAGCGCGTCTCACTGTGTTCAAAGTTCTGCGAAG

 TGGGGAGTGAGGGAAAGCGGTTACGAGTGACTTGGCTGGAGCCTCAGGGCGGGACTGG
 2041 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2100
 ACCCCTCACTCCCTCGCCAATGCTACTGAACCGACCTCGGAGTCCCCGCCGTGACC

 CACGGAACACACCCCTGAGGCCAGCCCTGGCTGCCAGGCCAGCTGCCCTTCTCCCG
 2101 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2160
 GTGCCCTGTGTTGGGACTCCGGTGGACCGACGGGTCGCCCTCGACGGAGAAGAGGGCGC

 GGTTGGTGGACCCGCTCAGTACGGAGTTGGGAAGCTTTCACTTCGGAGGATTGCTCA
 2161 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2220
 CCAACCACCTGGCGAGTCATGCCCTCAACCCCTCGAGAAAGTGAAGCCTCTAACGAGT

 ACAACCATGCTGGCATCTGGACCCCTCTACCTCTGGTGTACCCCTCCTGCCGGGTGG
 2221 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2280
 TGTGGTACGACCGTAGACCTGGGAGGATGGAGACCACTAGGGAGAGGACGGGCCACC

 AGGCTTACCCGCTTGTAGCTCCGGGATAGGCAAAGTGGGGCGGGACGCCGTGCG
 2281 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2340
 TCCGAATGGGGCAGAATCAGGGCCCTATCGTTCAACCCGCCGCGCCCTGCGCACGC

 GGATTGCGCGGCAGCGCGCACGCCGGCACCTGGAGCGCCGGCTGCTGCCGGAGGCG
 2341 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2400
 CCTAACGCCCGCTGCCCGTGCCTGCCGTGGACCCCTGCCGCCGACGACGCCCTCCGC

 TTGGAGACTGGCTCCGGGGCTGTTAGGACCTTCCCTCAGGCCGGTGCTCAGAACGA
 2401 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2460
 AACCTCTGACCGAGGGCCCCCGACAATCCTGAAAGGGAGTCCGGGCCACGAGTCTTGCT

 TGGAGGACTTGCTTTCTGGCCTTGATGCGAAGTGCTGATCCCGCTGGCAGGCCGGGG
 2461 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2520
 ACCTCCTGAACGAAAAGAACCGGAACACGCTTACGACTAGGGCAGCCGCTCCGCC

 CAGCTCCGGCGCTCTGGAGGACCAACTGCGCTCCACGTTGAGGTGGCGTGGGGGGCGGA
 2521 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2580
 GTCGAGGCCGCGAGGAGCTCTGGTACGCGAGGTGCAACTCCACCCGCCACCCCCCGCCT

 CAGGAATTGAAGCGGAAGTCTGGGAAGCTTTAGGGTGCCTGGAGGGGGACCCCGTTGGA
 2581 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2640
 GTCCCTTAACCTCGCCTCAGACCCCTCGAAATCCAGCGACCTCCCCCTGGGCCAACCT

<---- 4.p53-BE ---->
 (intron)

GAGAGGAGCGGAACCTCTGGACAAGCCCTGACAAGCCAAGCCAAAGGTCCGCTCCGGCGC
 2641 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2700
 CTCTCCTCGCCTTGAGGACCTGTTGGACTGTTGGTTCCAGGCGAGGCCGCG

Fig. 10C

2701 GGGTGGGTGAGTGC~~G~~C~~G~~CCCCGCGGGGGAGAGAGCCTACAGC~~T~~TCAGAAC~~A~~
 2761 CCCACCCACTCACCGCGGGCGCCCCCGCCCTCTCTCGGATGT~~CG~~GA~~G~~TCTTGT
 CATATTGCTCATTTCTGGCAGTTCTCAGAC~~G~~TAGGAATAAGTCAGCACC~~G~~AAGCAGTG
 2821 GTATAACGAGTAAAGACCGTCAAGAGTCTGCATCCTTATTCA~~G~~T~~C~~GTGGCTTCGT~~C~~AC
 GTTAAGCCGGAGGGCTCGGAAGAACGCCAC~~T~~TTCTTCGAAAAAGTTATATGGGG
 2881 CAATT~~C~~GGC~~T~~CCCGAGC~~T~~CTTGCCGTGAAAAGAAAGCTTTCAATATAACCCC
 CTGAATGAGCTTC~~G~~AGGCTTACCGTTTTATTGTCACACAGAAAAGGAACTG
 2941 GACTTACTCGAAGACCTCGAACAAATGGCAAAAATAACAGTGTGTCTT~~C~~TTGAC
 CCTTG~~T~~CTCC~~T~~CCGGGAATTCTCTTTAAGACTGTAAGTC~~G~~C~~T~~GAGTGGTTTC
 3001 TAAACACAAAACAAAAGACGGAAAGAGAAAAGAAAACGGAAAGAAC~~T~~GAACGTGAGG
 ATTTGTTTGT~~T~~CTGCC~~T~~CTCTTCTTTGCC~~T~~CTTAGCTTGCACTCC
 3061 CATGGTATTCTGCTTGGCTCCTGCTGGGTTGGTGGTACTCGTTCCACCGCACAGA
 GTACCACTAAAGACGAACCAGAGGACGACCCAAACCACCATGAGCAAGGGTGGCGTGTCT
 ACCCGGGCCTATTATGGCAAGAAACTTGAGCAGCCTGTTGAAAAGTCCCTCGCTC
 3121 TGGGCCGCGATAATAACCGGTCTTGAAC~~T~~CGTC~~G~~GA~~C~~AAA~~A~~CTTCAGGGAGCGAG
 AGAAATGCCAGCTTGCAGATGGCTAATCAAAG
 3181 TCTTACGGTCGAACGTCTACCGATTAGTT~~C~~
 3212

Fig. 10D

Fig. 11A

variations in the p53 binding region of figure 8

1. p1140 IMI

p1140	GGACAAGCCCTGACAAGCCA
p1140 IMI	GGAA <u>A</u> GCCCTGACAAGCCA ↑

positions of the mutations (boldface and arrow): **2270** (C→A)

2. p1140 IMII

p1140 GGACAAGCCCTGACAAGCCA
 p1140 IMII GGAAAGCCCTGAAAGCCA
 ↑ ↑

positions of the mutations (boldface and arrow): 2270 (C→A)
2280 (C→A)

3. p1140 MMK

p1140 GGACAAGCCCTGACAAGCCA
 p1140 IMIII GGAAAATCCCTGA~~AA~~ATCCA
 ↑↑↑↑

positions of the mutations (boldface and arrow): 2270 (C→A)
2273 (G→T)
2280 (C→A)
2283 (G→T)

Fig. 11B

4. p1140 IMIV

p1140 GGACAAGCCCTGACAAGCCA

p1140 IMIV **GCACAAGCCCT**CACAAGCCA
 ↑ ↑

positions of the mutations (boldface and arrow): 2268 (G→T)
 2278 (C→A)

Fig. 12A

variations in the p53 binding regions of figure 9

1. p1141 IMIII

p1141	GGACAAGCCCTGACAAGCCA
p1141 IMIII	GGAA AATCCCTGA AA ATCCA
	↑ ↑ ↑ ↑

positions of the mutations (boldface and arrow): 2270

2273

2280

2283

2. p1141 1p53

p1141	AGAGATGCCAAACTGTTTT
p1141 1p53	AGAGAT CCC AAA ATGTTTT
	↑ ↑

positions of the mutations (boldface and arrow): 50

57

3. p1141 2p53

p1141	AATGTTGCTTAAGCTTTTT
p1141 2p53	AATGTT CTTAAGATTTTTT
	↑ ↑

positions of the mutations (boldface and arrow): 443

450

Fig. 12B

4. p1141 3p53

p1141 AACTACCTAAGAGCTATCT

p1141 3p53 ACAATACCTAAGAGCTATCT

1

positions of the mutations (boldface and arrow): 1268 (A→C)
1270 (C→A)

5. p1141 ΔBgl

<---- 1.p53-BE ---->
p1141 AATAACCTTTAGAGATGCCAAACTGTTTCCCCAGAAC
p1141ΔBgl AATAACCTTTA-----GATCTCCCCAGAAC

6. p1141 ΔSpe

p1141 <---- 2.p53-BE ---->
 p1141 Δ Bgl CATTTGCCAATGGCTTAACTTTTGGCTACATTT
 p1141 Δ Bgl CATTTGCCA-----CTAGTGGCTACATTT

7. p1141 ΔMph

<---- 3.p53-BE ---->

p1141	AATTCA <u>GCTAA</u> ACTACCTAAGAGCTATCTACCGTTCCAA
p1141 Δ Bgl1	AATTCA <u>GCTATGCA</u> -----TACCGTTCCAA

Fig. 13A

variations in the p53 binding region of figure 10

1. p1142 TAG

mutation of the positions: 2227 (A→T)
2228 (T→A)

2. p1142 IMIII

p1142	GGACAAGCCCTGACAAGCCA
p1142 IMIII	GGAAAATCCCTGAAAATCCA ↑ ↑ ↑ ↑

positions of the mutations (boldface and arrow): 2662 (C→A)
2665 (G→T)
2672 (C→A)
2675 (G→T)

3. p1142 ΔBgl

<---- 1.p53-BE ---->	
p1142	AATAACCTT A GAGATGCC A ACTGTTTCCCCAGAACCA
p1142ΔBgl	AATAACCTT A ----- G ATCTCCCCAGAACCA

4. p1142 ΔSpe

<---- 2.p53-BE ---->	
p1142	CATCTTGCC A ATGTTGC T TAAGCTTTGGCTACATT
p1142ΔBgl	CATCTTGCC A ----- C TAGTGGCTACATT

Fig. 13B

5. p1142 ΔMph

<---- 3.p53-BE ---->

p1142	AATTCA <u>TGCTAA</u> ACTACCTAAGAGCTATCTACCGTTCCAA
p1142ΔBgl	AATTCA <u>TGCTATGCA</u> -----TACCGTTCCAA

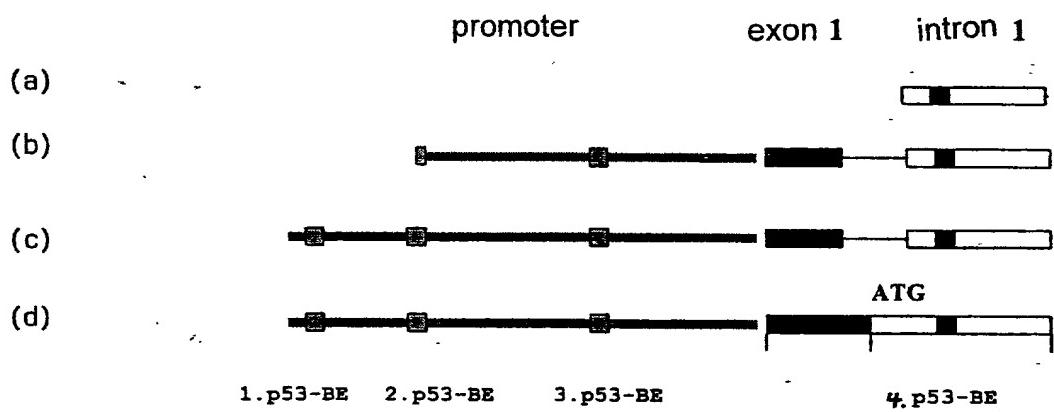


Fig. 14